```
> O V
O| |O   IntelliGenetics
> O V

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq72-t48453.res made by bobryen on Tue 17 Dec 102 12:58:03-PST.

Query sequence being compared:SEQ72-T48453 (1-151)
Number of sequences searched:                5
Number of scores above cutoff:               5

Results of the initial comparison of SEQ72-T48453 (1-151) with:
     File : seq72compares.pep
```

(histogram of scores)

```
                                                    Init. Opt.
Sequence Name    Description                  Length Score Score  Sig. Frame

  1. q9sr66         T22K18.18 protein.          1309   125   137   0.88    0
  2. t48453         TOIG of: t48453  check: 2431  555   124   134   0.86    0
```

```
1. SEQ72-T48453 (1-151)
   q9sr66         T22K18.18 protein.

Initial Score    =  125    Optimized Score      =  137    Significance =  0.88
Residue Identity =  52%    Matches              =  80     Mismatches   =  68
Gaps             =  0      Conservative Substitutions    =  3
```

(alignment sequences, residues 10–960, q9sr66 vs t48453)

```
2. SEQ72-T48453 (1-151)
   t48453    TOIG of: t48453   check: 2431   from: 1   to: 555

Initial Score    =  124    Optimized Score      =  134    Significance =  0.86
Residue Identity =  61%    Matches              =  84     Mismatches   =  53
Gaps             =  0      Conservative Substitutions    =  0
```

(alignment sequences, residues 10–550)

```
                    PARAMETERS
Similarity matrix   PAM-150        K-tuple            1
Threshold level of sim.  16%       Joining penalty    20
Mismatch penalty    1              Window size        151
Gap penalty         5.00
Gap size penalty    0.05
Cutoff score        1
Randomization group 0
```

```
                    SEARCH STATISTICS
              Mean     Median    Standard Deviation
              87       42        43.25
       CPU                       Total Elapsed
Times: 00:00:00.00              00:00:00.00

Number of residues:            3817
Number of sequences searched:     5
Number of scores above cutoff:    5
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq72-q941x6.res made by bobryen on Tue 17 Dec 102 12:58:40-PST.

Query sequence being compared:SEQ72-Q941X6 (1-132)
Number of sequences searched:                    5
Number of scores above cutoff:                   5

   Results of the initial comparison of SEQ72-Q941X6 (1-132) with:
        File : seq72compares.pep
```

```
100-
    -
    -
    -
N   -
U 50-
M   -
B   -
E   -
R   -
    -
O   -
F 10-
    -
S 5-
E   -
Q   -                                        *
U   -
E   -                                              *  *  *
N   -                                              |  |  |
C   -                                              |  |  |
E 0-|---|---|---|---|---|---|---|---|---|---|---|---|
       0  11  22  33  44  56  67  78  89 100
SCORE 0  11  22  33  44  56  67  78  89 100
STDEV  -1  -1          0
```

```
              PARAMETERS

Similarity matrix      PAM-150
Threshold level of sim.   16%        K-tuple              1
Mismatch penalty            1        Joining penalty     20
Gap penalty              5.00        Window size        132
Gap size penalty         0.05
Cutoff score                0
Randomization group         0
```

```
              SEARCH STATISTICS

          Mean    Median    Standard Deviation
Scores:    69       30          36.96

          CPU              Total Elapsed
Times:  00:00:00.90        00:00:01.00

Number of residues:             3817
Number of sequences searched:      5
Number of scores above cutoff:     5
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                                Init.   Opt.
Sequence Name     Description                         Length   Score   Score   Sig.  Frame

1. q9sr66         T22K18.18 protein.                    1309    121     100    0.84    0
2. t48453         TOIG of: t48453   check: 2431          555    119      96    0.73    0
3. q941x6         Putative FPPsynthase1 (Fragme          119    115      93    0.65    0
```

```
1. SEQ72-Q941X6 (1-132)
   q9sr66          T22K18.18 protein.

Initial Score     =  100     Optimized Score         = 121     Significance =  0.84
Residue Identity  =  56%     Matches                 =  75     Mismatches   =    57
Gaps              =    1     Conservative Substitutions =            0

              x    10        20        30        40        50
    WXXXRXXXXEXXXXXDXDWXXRXXXXXXXXXIXXRGMNXXLAXRIXXF
                                   ||  |||     || ||
    SKESAKSTQKKSVDWDSERKEAESGGRKRERTERTMDTVDHKIAN1/IKRGMNNMLAERIKAF
    780       790       800       810       820       830       840

              60        70        80        90       100       110       120
    LXXXVXXHGXIDLEWLRXXPPDXAKXYLLSIXGLGLKSVECVRLLXLHXXAFPVDTN-GRIAVRLGWVPLQP
    ||   |||  | |  ||| |||  ||  ||| |||||||||||||||||   |||||| ||||||||||||
    LNRLVKKHGSIDLEWLRDVPPDXAKEYLLSINGLGLKSVECVRLLSLHQIAFPVDTNVGRIAVRLGWVPLQP
    850       860       870       880       890       900       910       920

              130 x
    LPXXXQXHX
    | |  |
    LPDELQMHLLELYELHYHMITFGKVFCTK
    930       940
```

```
2. SEQ72-Q941X6 (1-132)
   t48453          TOIG of: t48453   check: 2431   from: 1   to: 555

Initial Score     =   99     Optimized Score         =  119     Significance =  0.73
Residue Identity  =   54%     Matches                =   73     Mismatches   =    58
Gaps              =    1     Conservative Substitutions =            1

              x    10        20        30        40        50
    WXXXRXXXXEXXXXXDXDWXXRXXXXXXXXXIXXRGMNXXIAXRIXXF
                                   ||  |||     || ||
    MKGTLADGKKPTSQWDSLRKDVEGNEGRQERNKNNMDSIDYEAIRRASSEISEAIKERGMNNMLAVRIKDF
    400       410       420       430       440       450       460       470

              60        70        80        90       100       110       120
    LXXXVXXHGXIDLEWLRXXPPDXAKXYLLSIXGLGLKSVECVRLLXLHXXAFPVDTN-GRIAVRLGWVPLQP
    |    |||  ||| || ||| |||  ||  |||||||||||||||||   |||||| ||||||||||||
    LERIVKDHGGIDLEWLRESPPDKJKDYLLSIRGLGLKSVECVRLLTHNLAFPVDTNVGRIAVRMGWVPLQP
    480       490       500       510       520       530       540

              130 x
    LPXXXQXHX
    || |  |
    LPESLQLHLLEL
    550 x
```

```
3. SEQ72-Q941X6 (1-132)
   q941x6)         Putative FPPsynthase1 (Fragment).

Initial Score     =   93     Optimized Score         =  115     Significance =  0.65
Residue Identity  =   60%     Matches                =   72     Mismatches   =    46
Gaps              =    1     Conservative Substitutions =            0

              x    10        20        30        40        50        60        70
    WXXXRXXXXEXXXXXDXDWXXRXXXXXXXXXIXXRGMNXXLAXRIXXFLXXXVXXHGXIDLEWLRXXP
    ||   |    : |:||:||::|  :  |:::|   ||||||  ||:|:::|:||:|:|||||||:::|
    LGWCIEWQVQDDYLDWEAVRCADVDEIANTIKRGMNNVLAKRIKDFLNRLVREHGNIDLEWLRDVP
    x    10        20        30        40        50        60
```

```
> o <
o| |o   Intelligenetics
> o <

FastDB - Fast Pairwise Comparison of Sequences
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Results file seq72-o49498.res made by bobryen on Tue 17 Dec 102 12:59:47-PST.

Query sequence being compared:SEQ72-O49498 (1-217)
Number of sequences searched:                    5
Number of scores above cutoff:                   5

Results of the initial comparison of SEQ72-O49498 (1-217) with:
    File : seq72compares.pep
```

```
        *
100-
    -
 N  -
 U 50-              *
 M  -
 B  -
 E  -
 R    -                                                              *
 O 10-
 F  -
    -
 S  5-                                          *
 E  -
 Q  -
 U  -
 E  -                        *              *              *        ||  ||
 N  -                                                      96   110 124
 C  -                *                                             1   2
 E  -        *       83   0
 S  0-|| ||  |69     |55    |41     |28    |14    ||
SCORE 0  14  -1      -1     -2      -3     -4
STDEV -4
```

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%	Joining penalty	20
Mismatch penalty	1	Window size	217
Gap penalty	5.00		
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
Scores:	92	80	18.94

	CPU	Total Elapsed
Times:	00:00:00.01	00:00:00.00

```
Number of residues:              3817
Number of sequences searched:       5
Number of scores above cutoff:      5
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
                                                          Init. Opt.
Sequence Name    Description                   Length Score Score Sig. Frame

                 **** 1 standard deviation above mean ****
  1. q9sr66       T22K18.18 protein.              1309   161   161  1.69   0
                 **** 0 standard deviation from mean ****
  2. t48453       TOIG of: t48453  check.: 2431    555   104    95  0.16   0
  3. q941x6       Putative FPPsynthase1 (Frag      119    94    84 -0.42   0
  4. t05430       TOIG of: t05430  check: 9156     917   138    79 -0.69   0
  5. o49498       Hypothetical 106.3 kDa prote1    917   138    79 -0.69   0
```

```
1. SEQ72-O49498 (1-217)
   q9sr66      T22K18.18 protein.

Initial Score    =  124   Optimized Score =  161   Significance = 1.69
Residue Identity =  42%   Matches         =   93   Mismatches   =   86
Gaps             =   33   Conservative Substitutions =        5

SKESAKSTQKKSVDWDSLRKEAESGGRKRERTERTMDTVDWDALRCTDVHKIANIIIKRGMNNMLAERI
780    790    800    810    820    830    840

        x        10        20        30        40        50
WXXXRXXXXXEXXXXXRXXXXXXIXXRGXXXXXIXXRGXXXXXLAXRIXXX

XXXXXXXXXXFLXXXXVXXXGXIDLEWLRXXDSXXXXKXXLLSXXGXGLKSXECVRLLLXXXAFPVDTNVGRIA
850    860    870    880    890    900    910
          ||||| ||||||||| ||||||||||||||| |||||||||||||
-----KAFLNRLVKKHGSIDLEWLRDVPPDKAKEYLLSINGLGLKSVECVRLLSLHQIAFPVDTNVGRIA

VRLGLVPLEPLPXXVQMHQLFYPXXXXXQKXLWPRLCKLXQXTLYELHYQMITFGKXFCTKXXPNCNACPM
920    930    940
||||| || || ||  |||  |||||                 ||||| ||||||  |||||||||||||||
VRLGWVPLQPLPDELQMHLL------------ELYELHYMITFGKYFCTKVKPNCNACPM
                                 950

KVECKYFASAXVSSKXILEXX
200    210

KAECRHYSSARASARLALPEPEESDRTSVMIHERRSKRKPV
960    970    980    990    1000
```

```
2. SEQ72-O49498 (1-217)
   t48453      TOIG of: t48453  check: 2431  from: 1  to: 555

Initial Score    =   95   Optimized Score =  104   Significance = 0.16
Residue Identity =   41%  Matches         =   60   Mismatches   =   74
Gaps             =   10   Conservative Substitutions =        2

        x        10        20        30        40        50
WXXXRXXXXXEXXXXXDXXXXXRXXXXXXXIXXRGXXXXXXIXXRGXXXXXLAXRIXXX

MKGTLADGKKPTSQWDSLRKDVEGNEGRQERNKNNMDSIDYFAIRRASISEISEAIKERGMNNMIAVRI---
400    410    420    430    440    450    460

XXXXXXXXXXFLXXXVXXXGXIDLEWLRXXDSXXXXKXXLLSXXGXGLKSXECVRLLLXXXAFPVDTNVGRIA
470    480    490    500    510    520    530
         ||||||| |||||||| || ||||| ||||||||| |||||||||||||
-----KDFLERIVKDHGGIDLEWLRESPPDKADYLLSIRGLGLKSVECVRLLTLHNLAFPVDTNVGRIA

VRLGLVPLEPLPXXVQMHQLFYPXXXXXQKXLWPRLCKLXQ
130    140    150    160
||:|| || |||  |||  |||||
VRMGWVPLQPLPESLQLHLLEL
540    550
```

```
3. SEQ72-O49498 (1-217)
   q941x6      Putative FPPsynthase1 (Fragment).
```

```
> o <
o| |o  Intelligenetics
> o <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq72-t05430.res made by bobryen on Tue 17 Dec 102 12:59:17-PST.

Query sequence being compared:SEQ72-T05430 (1-217)
Number of sequences searched: 5
Number of scores above cutoff: 5

Results of the initial comparison of SEQ72-T05430 (1-217) with:
     File : seq72compares.pep

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 1 standard deviation above mean ****					
1. q9sr66	T22K18.18 protein.	1309	161	124	1.69	0
	**** 0 standard deviation from mean ****					
2. t48453	TOIG of: t48453 check: 2431	555	119	95	0.16	0
3. q941x6	Putative FPPsynthase1 (Fragme	119	84	84	-0.42	0
4. t05430	TOIG of: t05430 check: 9156	917	138	79	-0.69	0

1. SEQ72-T05430 (1-217)
   q9sr66   T22K18.18 protein.

Initial Score   = 124   Optimized Score   = 161   Significance = 1.69
Residue Identity = 42%   Matches   = 93   Mismatches   = 86
Gaps   = 33   Conservative Substitutions =   5

```
              X       X       10        20        30        40        50
              WXXXRXXXNSXXVEXXXXXDXXXXXRXXXXXIXXRGXXXXLAXRIXXX
    SKESAKSTQKKSVDWDSLRKEAESGGRKRERTERTMDIVDWDALRCTDVHKIANTLIKRGMNNMLAERI ---
    780       790       800       810       820       830       840

              60        70        80        90        100       110       120
    XXXXXXXXXFLXXXVXXXGXIDLEWLRXXDSXXXXXLLSXXGXGLKSXECVRLLXLXXXAFPVDTNVGRIA
            | ||||  |  ||||||||  |||||||||
    --KAFLNRLVKKHGSIDLEWLRDVPPDKAKEYLLSINGLGLKSVECVRLLSLHQIAFPVDTNVGRIA
    850       860       870       880       890       900       910

              130       140       150       160       170       180       190
    VRLGLVPLEPLPXXVQMHQLFXYPXXXXXQKXLMPRLCKLXQXTLYELHYQMITFGKXFCTKXXPNCNACPM
    |||  ||| |||          |||||||||||  ||||||||||
    VRLGWVPLQPLPDELQMHLL-------------ELYELHYHMITFGKVPCTKVKPNCNACPM
    920       930       940       950

              200       210
    KXECKYFASAXVSSKXLLEXX
    ||| ::|| |::
    KAECRHYSSARASARLALPEPEESDRTSVMHERRSKRKPV
    960       970       980       990       1000
```

2. SEQ72-T05430 (1-217)
   t48453   TOIG of: t48453 check: 2431   from: 1   to: 555

Initial Score   = 95   Optimized Score   = 104   Significance = 0.16
Residue Identity = 41%   Matches   = 95   Mismatches   = 60
Gaps   = 33   Conservative Substitutions =   10

```
              X       10        20        30        40        50
              WXXXRXXXXXDXXXXXXXIXXRGXXXXIXXRGXXXXXIXXRGXXXXLAXRIXXX
    MKGTLADGKKPTSQWDSLRKDVEGNEGRQERNKNNMDSIDYEAIRRASISEISEAIKERGMNNMLAVRI----
    400       410       420       430       440       450       460

              60        70        80        90        100       110       120
    XXXXXXXXXFLXXXVXXXGXIDLEWLRXXDSXXXXXXXIXXRGXXXXLXLXXXAFPVDTNVGRIA
            ||||  |  ||||||||  |||||||||
    ------KDFLERIVKDHGGIDLEWLRESPPDKAKDYLLSIRGLGLKSVECVRLLTLHNLAFPVDTNVGRIA
    470       480       490       500       510       520       530

              130       140       150
    VRLGLVPLEPLPXXVQMHQLFXYPXXXXXQKXLMPRLCKLXQ
    |||  ||| |||   ||::|
    VRMGWVPLQPLPESLQLHLLEL
    540       550
```

3. SEQ72-T05430 (1-217)
   q941x6   Putative FPPsynthase1 (Fragment).

```
100-
 N
 U  50-
 M
 B
 E
 R
 O  10-
 F
 S
 E   5-
 Q
 U
 E
 N
 C
 E
 S   0-
      |   |   |   |   |   |   |   |   |   |
SCORE 0  14  28  41  55  69  83  96 110 124
STDEV-4  -3  -2  -1   0   1      1   2
     -3                              2
```

PARAMETERS

Similarity matrix	PAM-150	K-tuple	1
Threshold level of sim.	16%		
Mismatch penalty	1	Joining penalty	20
Gap penalty	5.00	Window size	217
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

	Mean	Median	Standard Deviation
	92	80	18.94

Times:	CPU	Total Elapsed
	00:00:00.01	00:00:00.00

Number of residues: 3817
Number of sequences searched: 5
Number of scores above cutoff: 5

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
> 0 <
0| |0   IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq71-t05430.res made by bobryen on Tue 17 Dec 102 13:25:29-PST.

Query sequence being compared: SEQ71-T05430 (1-88)
Number of sequences searched:    4
Number of scores above cutoff:   4

Results of the initial comparison of SEQ71-T05430 (1-88) with:
   File : seq71compares.pep
```

```
Sequence Name      Description                                             Length   Init. Opt.
                                                                                    Score Score  Sig.  Frame

  1. t05430         TOIG of: t05430   check: 9156   from: 1   to: 917        917     64    86    0.99   0
```

```
1. SEQ71-T05430 (1-88)
   t05430 }        TOIG of: t05430   check: 9156   from: 1   to: 917

Initial Score      =   64    Optimized Score        =   86    Significance =  0.99
Residue Identity   = 70%     Matches                =   69    Mismatches   =   19
Gaps               =  10     Conservative Substitutions =  10               =   0
```

```
                      X         10        20        30        40
           KVXLDPETXXXWXVLM------------DDKXTXAKWXXERXXFXTRXDLFINRM
           | |:|||||:..:|.||          ||:|:||.||::::||::|:||:||||||
           LKINKKVTTMIKADKKLVTAKVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRM
           400       410       420       430       440       450       460

             50        60        70        80         X
           HXLQGNRXFXQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP
           |:.||||:|.:|||||||||||||||||| |::||||||:.||.:||
           HRLQGNRKFKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFPVDAREGLSYYIEEPQDAKSS
           470       480       490       500       510  X    520       530
```

```
       100-
           -
           -
           -
           -
        50-
           -
           -
           -
           -
        N  -
        U  -
        M  -
        B  -
        E  -
        R  -
           -
        O  -
        F 10-
           -
        S  -
        E 5-
        Q  -
        U  -
        E  -
        N  -
        C  -                                                *
        E  -                                              **
        S  0-
           -----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------
       SCORE 0|  |7     |14    |21    |28    |36    |43    |50    |57    |64
       STDEV -9  -8     -7     -6     -5     -4     -3     -2     -1     0     1
```

```
                          PARAMETERS

Similarity matrix    PAM-150     K-tuple                 1
Threshold level of sim.  16%
Mismatch penalty       1          Joining penalty        20
Gap penalty         1.00          Window size            88
Gap size penalty    0.05
Cutoff score           1
Randomization group    0

                  SEARCH STATISTICS

Scores:          Mean      Median     Standard Deviation
                  58         55              6.08

Times:            CPU                    Total Elapsed
            00:00:00.00                  00:00:00.00

Number of residues:                4350
Number of sequences searched:         4
Number of scores above cutoff:        4
```

```
The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
> O <
O| |O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq72-q9sr66.res made by bobryen on Tue 17 Dec 102 12:57:35-PST.

Query sequence being compared:SEQ72-Q9SR66 (1-208)
Number of sequences searched:                      5
Number of scores above cutoff:                     5

Results of the initial comparison of SEQ72-Q9SR66 (1-208) with:
         File : seq72compares.pep
```

Sequence Name   Description   Length   Init.   Opt.   Sig. Frame
                                     Score   Score

**** 1 standard deviation above mean ****

1. q9sr66   T22K18.18 protein.   1309   137   176   1.29   0

```
1. SEQ72-Q9SR66 (1-208)
   q9sr66           T22K18.18 protein.

Initial Score      =    137   Optimized Score    =   176   Significance = 1.29
Residue Identity   =    59%   Matches            =   124   Mismatches   =   61
Gaps               =           Conservative Substitutions =    23        Gaps = 0
```

```
                 x        10        20        30        40        50
           WXXXRXXXXXEXXXXXDTXDWXXXRXXXXXXXXXXXIXXRGMNXXLAXRIXX
           :.:.:.:|.;|::.;.::.|.;;||;|::.:::|::.;;.::|;|;;:;||:::
  KSKESAKSTQKKSVDWDSLRKEAESGGRKRERTERTMDTVDWDALRCTDVHKIANIIIKRGMNNMLAERIKA
  780       790   x 800       810       820       830       840

                 60        70        80        90       100       120
  FLXXXVXXHGXIDLEWLRXXPPDXAKXYLLSIXGLGLKSVECVRLLXLHXXAFPVDTNVGRIAVRLGWVPLQ
  ||::;.;:;|;||||||||:;|::|.;|;;||;||||||||||||;:;|||;;||||||||||||||||||||
  FLNRLVKKHGSIDLEWLRDVPPDKAKEYLLSINGLGLKSVECVRLLSLHQIAFPVDTNVGRIAVRLGWVPLQ
  850       860       870       880       890       900       910

                130       140       150       160       170       180       190
  PLPXXLQMHLLXXYPXXXXXQKLLWPRLCKLXQXTLYELHYHMITFGKXFCTKXXPNCNACPMKXXECRHYSS
  ||;.;!||||| |;|||;:|||;;:;||;:|||||;||||||||||||||;!;;.|||||||;;:|:||||||
  PLPDELQMHLL---------------------------ELYELHYHMITFGKVFCTKVFCKVKPNCNACPMKAECRHYSS
  920       930                          940       950       960

  200      X
  AXASARXALPXP
  |:|||;!|;||!|
  ARASARLALPEPEESDRTSVMIHERRSRKPV
  970       980       990      1000
```

```
                                                                         *
                                                                    *    |--- 137
                                                               *    |--- 122
                                                          *    |--- 107
                                                     *    |--- 91
                                                *    |--- 76
                                           *    |--- 61    1
100-                                            |--- 46    0
  -
  -
 50-                         *
  -
  -
  -
  -
 10-
  -
  5-
  -
  -
  -
  -
  0-
    |---|---|---|---|---|---|---|---|
SCORE 0   15   30   46   61   76   91  107  122  137
STDEV -2   -1

                        PARAMETERS

Similarity matrix      PAM-150   K-tuple              1
Threshold level of sim.  16%
Mismatch penalty          1      Joining penalty     20
Gap penalty            5.00      Window size        208
Gap size penalty       0.05
Cutoff score              1
Randomization group       0

                  SEARCH STATISTICS

Scores:        Mean      Median      Standard Deviation
                92         58             35.00

Times:         CPU                   Total Elapsed
          00:00:00.01              00:00:00.00

Number of residues:               3817
Number of sequences searched:        5
Number of scores above cutoff:       5

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq71-q95r66.res made by bobryen on Tue 17 Dec 102 11:48:05-PST.

Query sequence being compared: SEQ71-Q95R66 (1-90)
Number of sequences searched: 4
Number of scores above cutoff: 4

Results of the initial comparison of SEQ71-Q95R66 (1-90) with:
          File : seq71compares.pep

| Init. Opt.
| Sequence Name   Description   Length Score Score Sig. Frame
| --
| **** 1 standard deviation above mean ****
| 1. q9sr66   T22K18.18 protein.   1309   67   80   1.06   0

1. SEQ71-Q95R66 (1-90)
   (q9sr66)
                    T22K18.18 protein.

Initial Score   = 67   Optimized Score = 80   Significance = 1.06
Residue Identity   = 69%   Matches   = 69   Mismatches   = 20
Gaps   =   9   Conservative Substitutions = 1

              x   10   20   30   40
              KVXLDPETXXXWXLLM-------DXXDEEKXKWWXXERXXFXGRXNSPIAR
              ||:|||||;;;:|:||| |:;|||:|||;:|||;:||;;|||||||||
              YKKSYEEQKAIVKYSKKQKPKVQLDPETSRVWKLLMSSIDCDGVDGSDEEKRKWWEEERNMFHGRANSPIAR
              480   490   500   510   520   530   540

              50   60   70   80   90
              MRXVQGNRXFXPWKGSVVDSVVGVFLTQNV-DXSSSSAYMXLASXFP
              ||:|||||;|:;|||||||||||||||||| |;||||||;:||:;||
              MRVVQGNRTFSPWKGSVVDSVVGVFLTQNVADHSSSSAYMDLAAEFPVEWNFNKGSCHEEWGSSVTQ
              550   560   570   580   590   x 600   610
```



PARAMETERS

| Similarity matrix    | PAM-150     | K-tuple         |  1 |
| Threshold level of sim. | 16%      |                 |    |
| Mismatch penalty     | 1           | Joining penalty | 20 |
| Gap penalty          | 5.00        | Window size     | 90 |
| Gap size penalty     | 0.05        |                 |    |
| Cutoff score         | 1           |                 |    |
| Randomization group  | 0           |                 |    |

SEARCH STATISTICS

|         | Mean | Median | Standard Deviation |
|---------|------|--------|--------------------|
| Scores: | 59   | 54     | 7.55               |

| Times: | CPU          | Total Elapsed |
|--------|--------------|---------------|
|        | 00:00:00.00  | 00:00:00.00   |

Number of residues:            4350
Number of sequences searched:     4
Number of scores above cutoff:    4

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
> O <
O| |O   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq71-o49498.res made by bobryen on Tue 17 Dec 102 12:55:59-PST.

Query sequence being compared: SEQ71-O49498 (1-90)
Number of sequences searched: 4
Number of scores above cutoff: 4

Results of the initial comparison of SEQ71-O49498 (1-90) with:
      File : seq71compares.pep

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig. Score	Sig. Frame
1. t05430	TOIG of: t05430 check: 9156	917	66	80	0.90	0
2. o49498	Hypothetical 106.3 kDa protei	917	66	80	0.90	0

1. SEQ71-O49498 (1-90)
   t05430   TOIG of: t05430   check: 9156   from: 1 to: 917

Initial Score   =   66   Optimized Score   =   80   Significance =   0.90
Residue Identity   =   70%   Matches   =   69   Mismatches   =   21
Gaps   =   8   Conservative Substitutions =   =   0

```
                    x         10        20        30        40
          KVXLDPETXXXWXVLM------XXDDKXTXAKWXXERXXFXTRXDLFINRM
          ||  |||| | |||        | |||  |||  |||  | |||||||||
LKINKKVTTMIKADKKLVTAKVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRM
400       410       420       430       440       450       460
          50        60        70        80        90
HXLQGNRXFXQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP
| |||||| ||||||||||||||||||| ||  |||||| |||  ||
HRLQGNRKFKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFPVDAREGLSYYIEEPQDAKSS
470       480       490       500       510       X  520       530
```

2. SEQ71-O49498 (1-90)
   o49498   Hypothetical 106.3 kDa protein.

Initial Score   =   66   Optimized Score   =   80   Significance =   0.90
Residue Identity   =   70%   Matches   =   69   Mismatches   =   21
Gaps   =   8   Conservative Substitutions =   =   0

```
                    x         10        20        30        40
          KVXLDPETXXXWXVLM------XXDDKXTXAKWXXERXXFXTRXDLFINRM
          |!|||||  ||:|:|||      :;||:|:,:||;:|!:;||:||||||||
LKINKKVTTMIKADKKLVTAKVNLDPETIKEWDVLMVNDSPSRSYDDKETEAKWKKEREIFQTRIDLFINRM
400       410       420       430       440       450       460
          50        60        70        80        90
HXLQGNRXFXQWKGSVVDSVVGVFLTQN-TDXLSSNAFMXVAAXFP
|;|||;;;;||||||||||||||||||| ||  |||||;;||;||;||
HRLQGNRKFKQWKGSVVDSVVGVFLTQNTTDYLSSNAFMSVAAKFPVDAREGLSYYIEEPQDAKSS
470       480       490       500       510       X  520       530
```

```
     100-
          -
      50-  -
   N    -
   U    -
   M    -
   B    -
   E    -
   R    -
          -
   O  10-
   F    -
          -
   S   5-
   E    -
   Q    -
   U    -
   E    -
   N    -          **           *
   C    -
   E    -
   S    0-|---|---|---|---|---|---|---|---|---|---|---|---|---|
          -7  -8  -6  -7  -5  -4  -3  -2  -1   0  51  59  66
SCORE  0                  15  22  29  37  44
STDEV  -8
```

PARAMETERS

Similarity matrix   PAM-150   K-tuple   1
Threshold level of sim. 16%
Mismatch penalty   1   Joining penalty   20
Gap penalty   5.00   Window size   90
Gap size penalty   0.05
Cutoff score   1
Randomization group 0

SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
             60   56   6.65

Times: CPU   Total Elapsed
             00:00:00.00   00:00:00.00

Number of residues: 4350
Number of sequences searched: 4
Number of scores above cutoff: 4

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

```
> O <
O|.O   IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results.file seq71-q9sjq6.res made by bobryen on Tue 17 Dec 102 12:54:30-PST.

Query sequence being compared: SEQ71-Q9SJQ6 (1-90)
Number of sequences searched:                      4
Number of scores above cutoff:                     4

    Results of the initial comparison of SEQ71-Q9SJQ6 (1-90) with:
        File : seq71compares.pep
```

```
100-|

     |
     |
  N  |
  U 50-|
  M  |
  B  |
  E  |
  R  |

  O  |
  F 10-|

     |
  S  |
  E 5-|
  Q  |
  U  |
  E  |
  N  |
  C  |
  E  |
  S  0-|--|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
SCORE 0-| 7  15  22  29  37  44  51  59  66
STDEV  -8  -7  -6  -5  -4  -3  -2  -1   0   1
```

```
                    PARAMETERS

Similarity matrix    PAM-150    K-tuple              1
Threshold level of sim.  16%
Mismatch penalty        1       Joining penalty     20
Gap penalty          5.00       Window size         90
Gap size penalty     0.05
Cutoff score            1
Randomization group     0

                    SEARCH STATISTICS

Scores:           Mean     Median    Standard Deviation
                   59        55            6.65

Times:             CPU                  Total Elapsed
              00:00:00.00              00:00:00.00

Number of residues:           4350
Number of sequences searched:    4
Number of scores above cutoff:   4

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                     Init. Opt.
Sequence Name    Description          Length Score Score Sig. Frame
---------------  -----------          ------ ----- ----- ---- -----
                 **** 1 standard deviation above mean ****
   1. q9sjq6     At2g36490 protein.     1207    66    80  1.05   0


1. SEQ71-Q9SJQ6 (1-90)
   q9sjq6 :)    At2g36490 protein.

Initial Score     =    66   Optimized Score    =   80   Significance =  1.05
Residue Identity  =   69%   Matches            =   69   Mismatches   =   21
Gaps              =    9    Conservative Substitutions =    0

                  x          10        20        30        40
               KVXLDDETXXXWXLLL------DXXDEXKXKWWXXERXXFXGRXDSFIAR
               |:|:||||:;:;||||       |:;||:|:;||:|:;|;|:|||||||
          GGGAGAIVPVTPVKKPRPRPKVDLDDETDRVWKLLLENINSEGVDGSDEQKAKWEEERNVFRGRADSFIAR
          480       490       500       510       520       530       540       550

                  50        60        70        80      x
               MHXVQGDRXFXPWKGSVVDSVVGVFLTQNV-DXLSSSAFMXLASXFP
               ||:||||:|:||||||||||||||||||| | ||||||:;||:;||
               MHLVQGDRRFTPWKGSVVDSVVGVFLTQNVSDHLSSSAFMSLASQFPVPFVPSSNFDAGTSSMPSIQ
               560       570       580       590       600       610
```